Amendments to the Specification:

Please replace the paragraph starting on page 91 line 8 with the following amended paragraph:

Alignment of the *E. coli* and *Arabidopsis gcpE* proteins shows high similarity but also striking differences. The first 75 amino acid residues of the *Arabidopsis* sequence constitute a region that is not present in the bacterial counterpart. A transit peptide for plastids is predicted at this region with the ChloroP V1.0 program accessible at the Center for Biological Sequences, University of Denmark web site and described by Emanuelsson, *et al.* (*Protein Science* 8:978-984, (1999)) ~~www.cbs.dtu.dk/services/ChloroP/ (Score 0.53295)~~. According to this program, the processing site of the transit peptide would be located between Arg38 and Ser39 (CS-score 2.392). *In vivo* import experiments to chloroplasts demonstrated that the N-terminal region of the *Arabidopsis* protein is a functional transit peptide for plastids.

Please replace the paragraph starting on page 100 line 1 with the following amended paragraph:

Upon identification of the *Escherichia coli gcpE* gene as involved in the trunk line of the MEP pathway for isoprenoid biosynthesis, the available databases are searched for plant homologs. As described in Example 4, clone 135H1 (Genbank accession number T46582) is identified as containing an *Arabidopsis thaliana* cDNA encoding a protein with homology to the product of the bacterial *gcpE* gene. As shown in Figure 4, however, the putative *Arabidopsis* GCPE protein (SEQ ID NO: 79), contains several domains that are absent from the *E. coli* protein (SEQ ID NO: 78). Identical residues are in black boxes and conservative changes in grey boxes. Gaps are indicated with dots. The predicted cleavage site for the plastidial targeting peptide (according to the ChloroP program, accessible at the Center for Biological Sequences, University of Denmark web site and described by Emanuelsson, *et al.* (*Protein Science* 8:978-984, (1999)); ~~genome.cbs.dtu.dk/services/chlorop~~) is indicated with an arrow (*see* Figure 4).

Please replace the paragraph starting on page 108 line 9 with the following amended paragraph:

The multiple gene construct contains the *gcpE* gene and one or more genes for other MEP pathway proteins, including, but not limited to: a *ygbB* gene; a *ygbP* gene; a *ychB* gene; a *yfgA* gene; a *yfgB* gene; a bifunctional prephenate dehydrogenase such as the *E. herbicola* or *E. coli tyrA* gene (Xia *et al.*, *J. Gen. Microbiol.*, 138:1309-1316, 1992), a phytylprenyltransferase such as the slr1736 gene (in Cyanobase, a web accessible database maintained by Kazusa DNA Research Institute, Kisarazu, JAPAN ~~www.kazusa.or.jp/cyanobase~~) or the ATPT2 gene (Smith *et al.*, *Plant J.*, 11:83-92, 1997), a deoxyxylulose synthase such as the *E. coli dxs* gene (Lois *et al.*, *PNAS*, 95(5):2105-2110, 1998), a deoxyxylulose reductoisomerase such as the *dxr* gene (Takahashi *et al.*, *PNAS*, 95(17):9879-9884, 1998), an *Arabidopsis thaliana* HPPD gene (Norris *et al.*, *Plant Physiol.*, 117:1317-1323, 1998), an *Arabidopsis thaliana* GGPPS gene (Bartley and Scolnik, *Plant Physiol.*, 104:1469-1470, 1994), a transporter such as the AANT1 gene (Saint Guily, *et al.*, *Plant Physiol.*, 100(2):1069-1071, 1992), a GMT gene (WO 00/32757, WO 00/10380), an MT1 gene, a tocopherol cyclase such as the slr1737 gene (in Cyanobase) or its *Arabidopsis* ortholog, an isopentenyl diphosphate isomerase (IDI) gene, and an antisense construct for homogentisic acid dioxygenase (Sato *et al.*, *J. DNA Res.*, 7(1):31-63, 2000).